

AMENDMENTS TO THE SEQUENCE LISTING

The information for SEQ ID NO: 76 in the Sequence Listing has been amended as follows

(2) INFORMATION FOR SEQ ID NO: 76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) DESCRIPTION: 5' donor consensus splice sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

~~ATACAGGGCAT~~ CACAGGTATT A

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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant : Jan Zavada et al.

Serial No.: 09/772,719

Group Art Unit: 1634

Filed : January 30, 2001

Examiner: E.C. Whisenant

For : MN Gene and Protein

SUBMISSION OF SUBSTITUTE SEQUENCE LISTING

MAIL STOP AF
Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

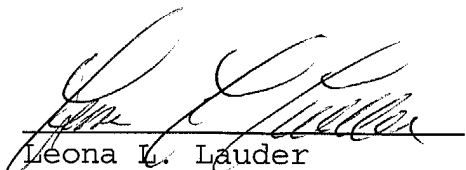
Sir:

Applicants submit the enclosed substitute Sequence Listing of the nucleotide and amino acid sequences contained in the above-identified application. Also enclosed is a computer readable copy of the substitute Sequence Listing. The nucleotide and amino acid sequences are presented in a form which conforms with the requirements of 37 CFR Sections 1.821 through 1.825.

In accordance with 37 CFR Section 1.821(f), the undersigned Attorney for the Applicants hereby states that the information recorded in computer readable form is identical to that in the printed substitute Sequence Listing. Further, in accordance with 37 CFR Section 1.821(g), the undersigned Attorney

for the Applicants states that the enclosed substitute Sequence Listing includes no new matter.

Respectfully submitted,



Leona L. Lauder
Attorney for Applicants
Registration No. 30,863

Dated: December 3, 2003



SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Zavada, Jan
Pastorekova, Silvia
Pastorek, Jaromir

(ii) TITLE OF INVENTION: MN Gene and Protein

(iii) NUMBER OF SEQUENCES: 86

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Leona L. Lauder
(B) STREET: 465 California Street, Suite 450
(C) CITY: San Francisco
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94104

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 09/772,719
(B) FILING DATE: 30-JAN-2001
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/485,049
(B) FILING DATE: 07-JUN-1995

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Lauder, Leona L.
(B) REGISTRATION NUMBER: 30,863
(C) REFERENCE/DOCKET NUMBER: D-0021.3A-2

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 415-981-2034
(B) TELEFAX: 415-981-0332

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1522 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ACAGTCAGCC GCATGGCTCC CCTGTGCCCC AGCCCCTGGC TCCCTCTGTT GATCCCGGCC	60
CCTGCTCCAG GCCTCACTGT GCAACTGCTG CTGTCACTGC TGCTTCTGAT GCCTGTCCAT	120
CCCCAGAGGT TGCCCCGGAT GCAGGAGGAT TCCCCCTTGG GAGGAGGCTC TTCTGGGGAA	180
GATGACCCAC TGGGCGAGGA GGATCTGCCC AGTGAAGAGG ATTCACCCAG AGAGGAGGAT	240
CCACCCGGAG AGGAGGATCT ACCTGGAGAG GAGGATCTAC CTGGAGAGGA GGATCTACCT	300
GAAGTTAAGC CTAAATCAGA AGAAGAGGGC TCCCTGAAGT TAGAGGATCT ACCTACTGTT	360
GAGGCTCCTG GAGATCCTCA AGAACCCAG AATAATGCCC ACAGGGACAA AGAAGGGGAT	420
GACCAGAGTC ATTGGCGCTA TGGAGGCGAC CCGCCCTGGC CCCGGGTGTC CCCAGCCTGC	480
GCGGGCCGCT TCCAGTCCCC GGTGGATATC CGCCCCCAGC TCGCCGCCTT CTGCCCCGCC	540
CTGCGCCCCC TGGAATCCT GGGCTTCCAG CTCCCGCCGC TCCAGAACT GCGCCTGCGC	600
AACAATGGCC ACAGTGTGCA ACTGACCCTG CCTCCTGGGC TAGAGATGGC TCTGGGTCCC	660
GGGCGGGAGT ACCGGGCTCT GCAGCTGCAT CTGCACTGGG GGGCTGCAGG TCGTCCGGGC	720
TCGGAGCACA CTGTGGAAGG CCACCGTTTC CCTGCCGAGA TCCACGTGGT TCACCTCAGC	780
ACCGCCTTTG CCAGAGTTGA CGAGGCCTTG GGGCGCCCGG GAGGCCTGGC CGTGTTGGCC	840
GCCTTTCTGG AGGAGGGCCC GGAAGAAAAC AGTGCCTATG AGCAGTTGCT GTCTCGCTTG	900
GAAGAAATCG CTGAGGAAGG CTCAGAGACT CAGGTCCCAG GACTGGACAT ATCTGCACTC	960
CTGCCCTCTG ACTTCAGCCG CTAATTCCAA TATGAGGGGT CTCTGACTAC ACCGCCCTGT	1020
GCCCAGGGTG TCATCTGGAC TGTGTTTAAC CAGACAGTGA TGCTGAGTGC TAAGCAGCTC	1080
CACACCCTCT CTGACACCCT GTGGGGACCT GGTGACTCTC GGCTACAGCT GAACTTCCGA	1140
GCGACGCAGC CTTTGAATGG GCGAGTGATT GAGGCCTCCT TCCCTGCTGG AGTGGACAGC	1200
AGTCCTCGGG CTGCTGAGCC AGTCCAGCTG AATTCCTGCC TGGCTGCTGG TGACATCCTA	1260
GCCCTGGTTT TTGGCCTCCT TTTTGCTGTC ACCAGCGTCG CGTTCCTTGT GCAGATGAGA	1320
AGGCAGCACA GAAGGGGAAC CAAAGGGGGT GTGAGCTACC GCCCAGCAGA GGTAGCCGAG	1380
ACTGGAGCCT AGAGGCTGGA TCTTGAGAA TGTGAGAAGC CAGCCAGAGG CATCTGAGGG	1440
GGAGCCGGTA ACTGTCCTGT CCTGCTCATT ATGCCACTTC CTTTAACTG CCAAGAAATT	1500
TTTTAAAATA AATATTTATA AT	1522

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 459 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- (A) DESCRIPTION: First 37 amino acids represent signal peptide, and remaining amino acids represent mature protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met	Ala	Pro	Leu	Cys	Pro	Ser	Pro	Trp	Leu	Pro	Leu	Leu	Ile	Pro	Ala	
	-35					-30					-25					
Pro	Ala	Pro	Gly	Leu	Thr	Val	Gln	Leu	Leu	Leu	Ser	Leu	Leu	Leu	Leu	
	-20				-15						-10					
Met	Pro	Val	His	Pro	Gln	Arg	Leu	Pro	Arg	Met	Gln	Glu	Asp	Ser	Pro	
-5					1				5					10		
Leu	Gly	Gly	Gly	Ser	Ser	Gly	Glu	Asp	Asp	Pro	Leu	Gly	Glu	Glu	Asp	
			15				20						25			
Leu	Pro	Ser	Glu	Glu	Asp	Ser	Pro	Arg	Glu	Glu	Asp	Pro	Pro	Gly	Glu	
		30					35					40				
Glu	Asp	Leu	Pro	Gly	Glu	Glu	Asp	Leu	Pro	Gly	Glu	Glu	Asp	Leu	Pro	
	45					50					55					
Glu	Val	Lys	Pro	Lys	Ser	Glu	Glu	Glu	Gly	Ser	Leu	Lys	Leu	Glu	Asp	
60					65					70					75	
Leu	Pro	Thr	Val	Glu	Ala	Pro	Gly	Asp	Pro	Gln	Glu	Pro	Gln	Asn	Asn	
				80					85					90		
Ala	His	Arg	Asp	Lys	Glu	Gly	Asp	Asp	Gln	Ser	His	Trp	Arg	Tyr	Gly	
			95					100					105			
Gly	Asp	Pro	Pro	Trp	Pro	Arg	Val	Ser	Pro	Ala	Cys	Ala	Gly	Arg	Phe	
		110					115					120				
Gln	Ser	Pro	Val	Asp	Ile	Arg	Pro	Gln	Leu	Ala	Ala	Phe	Cys	Pro	Ala	
	125					130					135					
Leu	Arg	Pro	Leu	Glu	Leu	Leu	Gly	Phe	Gln	Leu	Pro	Pro	Leu	Pro	Glu	
140					145					150					155	
Leu	Arg	Leu	Arg	Asn	Asn	Gly	His	Ser	Val	Gln	Leu	Thr	Leu	Pro	Pro	
				160					165					170		

Gly	Leu	Glu	Met	Ala	Leu	Gly	Pro	Gly	Arg	Glu	Tyr	Arg	Ala	Leu	Gln	175	180	185
Leu	His	Leu	His	Trp	Gly	Ala	Ala	Gly	Arg	Pro	Gly	Ser	Glu	His	Thr	190	195	200
Val	Glu	Gly	His	Arg	Phe	Pro	Ala	Glu	Ile	His	Val	Val	His	Leu	Ser	205	210	215
Thr	Ala	Phe	Ala	Arg	Val	Asp	Glu	Ala	Leu	Gly	Arg	Pro	Gly	Gly	Leu	220	225	230
Ala	Val	Leu	Ala	Ala	Phe	Leu	Glu	Glu	Gly	Pro	Glu	Glu	Asn	Ser	Ala	240	245	250
Tyr	Glu	Gln	Leu	Leu	Ser	Arg	Leu	Glu	Glu	Ile	Ala	Glu	Glu	Gly	Ser	255	260	265
Glu	Thr	Gln	Val	Pro	Gly	Leu	Asp	Ile	Ser	Ala	Leu	Leu	Pro	Ser	Asp	270	275	280
Phe	Ser	Arg	Tyr	Phe	Gln	Tyr	Glu	Gly	Ser	Leu	Thr	Thr	Pro	Pro	Cys	285	290	295
Ala	Gln	Gly	Val	Ile	Trp	Thr	Val	Phe	Asn	Gln	Thr	Val	Met	Leu	Ser	300	305	310
Ala	Lys	Gln	Leu	His	Thr	Leu	Ser	Asp	Thr	Leu	Trp	Gly	Pro	Gly	Asp	320	325	330
Ser	Arg	Leu	Gln	Leu	Asn	Phe	Arg	Ala	Thr	Gln	Pro	Leu	Asn	Gly	Arg	335	340	345
Val	Ile	Glu	Ala	Ser	Phe	Pro	Ala	Gly	Val	Asp	Ser	Ser	Pro	Arg	Ala	350	355	360
Ala	Glu	Pro	Val	Gln	Leu	Asn	Ser	Cys	Leu	Ala	Ala	Gly	Asp	Ile	Leu	365	370	375
Ala	Leu	Val	Phe	Gly	Leu	Leu	Phe	Ala	Val	Thr	Ser	Val	Ala	Phe	Leu	380	385	390
Val	Gln	Met	Arg	Arg	Gln	His	Arg	Arg	Gly	Thr	Lys	Gly	Gly	Val	Ser	400	405	410
Tyr	Arg	Pro	Ala	Glu	Val	Ala	Glu	Thr	Gly	Ala						415	420	

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CGCCCAGTGG GTCATCTTCC CCAGAAGAG

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(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

GGAATCCTCC TGCATCCGG

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(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10898 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

GGATCCTGTT GACTCGTGAC CTTACCCCCA ACCCTGTGCT CTCTGAAACA TGAGCTGTGT 60

CCACTCAGGG TTAAATGGAT TAAGGGCGGT GCAAGATGTG CTTTGTTAAA CAGATGCTTG 120

AAGGCAGCAT GCTCGTTAAG AGTCATCACC AATCCCTAAT CTCAAGTAAT CAGGGACACA 180

AACACTGCGG AAGGCCGCAG GGTCCCTCTGC CTAGGAAAAC CAGAGACCTT TGTTCACCTG 240

TTTATCTGAC CTTCCCTCCA CTATTGTCCA TGACCCTGCC AAATCCCCCT CTGTGAGAAA 300

CACCCAAGAA TTATCAATAA AAAAATAAAT TTAAAAAAA AATACAAAAA AAAAAAAAAA 360

AAAAAAAAAA	GACTTACGAA	TAGTTATTGA	TAAATGAATA	GCTATTGGTA	AAGCCAAGTA	420
AATGATCATA	TTCAAAACCA	GACGGCCATC	ATCACAGCTC	AAGTCTACCT	GATTTGATCT	480
CTTTATCATT	GTCATTCTTT	GGATTCACTA	GATTAGTCAT	CATCCTCAAA	ATTCTCCCCC	540
AAGTTCTAAT	TACGTTCCAA	ACATTTAGGG	GTTACATGAA	GCTTGAACCT	ACTACCTTCT	600
TTGCTTTTGA	GCCATGAGTT	GTAGGAATGA	TGAGTTTACA	CCTTACATGC	TGGGGATTAA	660
TTTAAACTTT	ACCTCTAAGT	CAGTTGGGTA	GCCTTTGGCT	TATTTTTGTA	GCTAATTTTG	720
TAGTTAATGG	ATGCACTGTG	AATCTTGCTA	TGATAGTTTT	CCTCCACACT	TTGCCACTAG	780
GGGTAGGTAG	GTACTCAGTT	TTCAGTAATT	GCTTACCTAA	GACCCTAAGC	CCTATTTCTC	840
TTGTACTGGC	CTTTATCTGT	AATATGGGCA	TATTTAATAC	AATATAATTT	TTGGAGTTTT	900
TTTGTTTGTT	TGTTTGTTTT	TTTTTTTGAG	ACGGAGTCTT	GCATCTGTCA	TGCCCAGGCT	960
GGAGTAGCAG	TGGTGCCATC	TCGGCTCACT	GCAAGCTCCA	CCTCCCGAGT	TCACGCCATT	1020
TTCTGCCTC	AGCCTCCCGA	GTAGCTGGGA	CTACAGGCGC	CCGCCACCAT	GCCCCGGCTAA	1080
TTTTTTGTAT	TTTTGGTAGA	GACGGGGTTT	CACCGTGTTA	GCCAGAATGG	TCTCGATCTC	1140
CTGACTTCGT	GATCCACCCG	CCTCGGCCTC	CCAAAGTTCT	GGGATTACAG	GTGTGAGCCA	1200
CCGCACCTGG	CCAATTTTTT	GAGTCTTTTA	AAGTAAAAAT	ATGTCTTGTA	AGCTGGTAAC	1260
TATGGTACAT	TTCTTTTTAT	TAATGTGGTG	CTGACGGTCA	TATAGGTTCT	TTTGAGTTTG	1320
GCATGCATAT	GCTACTTTTT	GCAGTCCTTT	CATTACATTT	TTCTCTCTTC	ATTTGAAGAG	1380
CATGTTATAT	CTTTTAGCTT	CACTTGGCTT	AAAAGGTTCT	CTCATTAGCC	TAACACAGTG	1440
TCATTGTTGG	TACCACTTGG	ATCATAAGTG	GAAAAACAGT	CAAGAAATTG	CACAGTAATA	1500
CTTGTTTGTA	AGAGGGATGA	TTCAGGTGAA	TCTGACACTA	AGAAACTCCC	CTACCTGAGG	1560
TCTGAGATTC	CTCTGACATT	GCTGTATATA	GGCTTTTCCT	TTGACAGCCT	GTGACTGCGG	1620
ACTATTTTTC	TTAAGCAAGA	TATGCTAAAG	TTTTGTGAGC	CTTTTTCCAG	AGAGAGGTCT	1680
CATATCTGCA	TCAAGTGAGA	ACATATAATG	TCTGCATGTT	TCCATATTTT	AGGAATGTTT	1740
GCTTGTGTTT	TATGCTTTTA	TATAGACAGG	GAAACTTGTT	CCTCAGTGAC	CCAAAAGAGG	1800
TGGGAATTGT	TATTGGATAT	CATCATTGGC	CCACGCTTTC	TGACCTTGGA	AACAATTAAG	1860
GGTTCATAAT	CTCAATTCTG	TCAGAATTGG	TACAAGAAAT	AGCTGCTATG	TTTCTTGACA	1920
TTCCACTTGG	TAGGAAATAA	GAATGTGAAA	CTCTTCAGTT	GGTGTGTGTC	CCTNGTTTTT	1980
TTGCAATTTT	CTTCTTACTG	TGTTAAAAAA	AAGTATGATC	TTGCTCTGAG	AGGTGAGGCA	2040

TTCTTAATCA	TGATCTTTAA	AGATCAATAA	TATAATCCTT	TCAAGGATTA	TGTCTTTATT	2100
ATAATAAAGA	TAATTTGTCT	TTAACAGAAT	CAATAATATA	ATCCCTTAAA	GGATTATATC	2160
TTTGCTGGGC	GCAGTGGCTC	ACACCTGTAA	TCCCAGCACT	TTGGGTGGCC	AAGGTGGAAG	2220
GATCAAATTT	GCCTACTTCT	ATATTATCTT	CTAAAGCAGA	ATTCATCTCT	CTTCCCTCAA	2280
TATGATGATA	TTGACAGGGT	TTGCCCTCAC	TCACTAGATT	GTGAGCTCCT	GCTCAGGGCA	2340
GGTAGCGTTT	TTTGTTTTTG	TTTTTGTTTT	TCTTTTTTGA	GACAGGGTCT	TGCTCTGTCA	2400
CCCAGGCCAG	AGTGCAATGG	TACAGTCTCA	GCTCACTGCA	GCCTCAACCG	CCTCGGCTCA	2460
AACCATCATC	CCATTTCAGC	CTCCTGAGTA	GCTGGGACTA	CAGGCACATG	CCATTACACC	2520
TGGCTAATTT	TTTTGTATTT	CTAGTAGAGA	CAGGGTTTGG	CCATGTTGCC	CGGGCTGGTC	2580
TCGAACTCCT	GGACTCAAGC	AATCCACCCA	CCTCAGCCTC	CCAAAATGAG	GGACCGTGTC	2640
TTATTCATTT	CCATGTCCCT	AGTCCATAGC	CCAGTGCTGG	ACCTATGGTA	GTACTAAATA	2700
AATATTTGTT	GAATGCAATA	GTAAATAGCA	TTTCAGGGAG	CAAGAACTAG	ATTAACAAAG	2760
GTGGTAAAAG	GTTTGGAGAA	AAAAATAATA	GTTTAATTTG	GCTAGAGTAT	GAGGGAGAGT	2820
AGTAGGAGAC	AAGATGGAAA	GGTCTCTTGG	GCAAGGTTTT	GAAGGAAGTT	GGAAGTCAGA	2880
AGTACACAAT	GTGCATATCG	TGGCAGGCAG	TGGGGAGCCA	ATGAAGGCTT	TTGAGCAGGA	2940
GAGTAATGTG	TTGAAAAATA	AATATAGGTT	AAACCTATCA	GAGCCCCTCT	GACACATACA	3000
CTTGCTTTTC	ATTCAAGCTC	AAGTTTGTCT	CCCACATAAC	CATTACTTAA	CTCACCTCG	3060
GGCTCCCCTA	GCAGCCTGCC	CTACCTCTTT	ACCTGCTTCC	TGGTGGAGTC	AGGGATGTAT	3120
ACATGAGCTG	CTTTCCTCT	CAGCCAGAGG	ACATGGGGGG	CCCCAGCTCC	CCTGCCTTTC	3180
CCCTTCTGTG	CCTGGAGCTG	GGAAGCAGGC	CAGGGTTAGC	TGAGGCTGGC	TGGCAAGCAG	3240
CTGGGTGGTG	CCAGGGAGAG	CCTGCATAGT	GCCAGGTGGT	GCCTTGGGTT	CCAAGCTAGT	3300
CCATGGCCCC	GATAACCTTC	TGCCTGTGCA	CACACCTGCC	CCTCACTCCA	CCCCATCCT	3360
AGCTTTGGTA	TGGGGGAGAG	GGCACAGGGC	CAGACAAACC	TGTGAGACTT	TGGCTCCATC	3420
TCTGCAAAAG	GGCGCTCTGT	GAGTCAGCCT	GCTCCCCTCC	AGGCTTGCTC	CTCCCCCACC	3480
CAGCTCTCGT	TTCCAATGCA	CGTACAGCCC	GTACACACCG	TGTGCTGGGA	CACCCACAG	3540
TCAGCCGCAT	GGCTCCCCTG	TGCCCCAGCC	CCTGGCTCCC	TCTGTTGATC	CCGGCCCCCTG	3600
CTCCAGGCCT	CACTGTGCAA	CTGCTGCTGT	CACTGCTGCT	TCTGGTGCCT	GTCCATCCCC	3660
AGAGGTTGCC	CCGGATGCAG	GAGGATTCCC	CCTTGGGAGG	AGGCTCTTCT	GGGGAAGATG	3720

ACCCACTGGG	CGAGGAGGAT	CTGCCCAGTG	AAGAGGATTC	ACCCAGAGAG	GAGGATCCAC	3780
CCGGAGAGGA	GGATCTACCT	GGAGAGGAGG	ATCTACCTGG	AGAGGAGGAT	CTACCTGAAG	3840
TTAAGCCTAA	ATCAGAAGAA	GAGGGCTCCC	TGAAGTTAGA	GGATCTACCT	ACTGTTGAGG	3900
CTCCTGGAGA	TCCTCAAGAA	CCCCAGAATA	ATGCCACAG	GGACAAAGAA	GGTAAGTGGT	3960
CATCAATCTC	CAAATCCAGG	TTCCAGGAGG	TTCATGACTC	CCCTCCCATA	CCCCAGCCTA	4020
GGCTCTGTTC	ACTCAGGGAA	GGAGGGGAGA	CTGTACTCCC	CACAGAAGCC	CTTCCAGAGG	4080
TCCCATACCA	ATATCCCCAT	CCCCACTCTC	GGAGGTAGAA	AGGGACAGAT	GTGGAGAGAA	4140
AATAAAAAGG	GTGCAAAAGG	AGAGAGGTGA	GCTGGATGAG	ATGGGAGAGA	AGGGGGAGGC	4200
TGGAGAAGAG	AAAGGGATGA	GAACTGCAGA	TGAGAGAAAA	AATGTGCAGA	CAGAGGAAAA	4260
AAATAGGTGG	AGAAGGAGAG	TCAGAGAGTT	TGAGGGGAAG	AGAAAAGGAA	AGCTTGAGG	4320
GTGAAGTGGG	TACCAGAGAC	AAGCAAGAAG	AGCTGGTAGA	AGTCATCTCA	TCTTAGGCTA	4380
CAATGAGGAA	TTGAGACCTA	GGAAGAAGGG	ACACAGCAGG	TAGAGAAACG	TGGCTTCTTG	4440
ACTCCCAAGC	CAGGAATTTG	GGGAAAGGGG	TTGGAGACCA	TACAAGGCAG	AGGGATGAGT	4500
GGGGAGAAGA	AAGAAGGGAG	AAAGGAAAGA	TGGTGTACTC	ACTCATTTGG	GA CTCAGGAC	4560
TGAAGTGCCC	ACTCACTTTT	TTTTTTTTTT	TTTTTGAGAC	AACTTTTCAC	TTTTGTTGCC	4620
CAGGCTGGAG	TGCAATGGCG	CGATCTCGGC	TCACTGCAAC	CTCCACCTCC	CGGGTTCAAG	4680
TGATTCTCCT	GCCTCAGCCT	CTAGCCAAGT	AGCTGCGATT	ACAGGCATGC	GCCACCACGC	4740
CCGGCTAATT	TTTGTATTTT	TAGTAGAGAC	GGGGTTTCGC	CATGTTGGTC	AGGCTGGTCT	4800
CGAACTCCTG	ATCTCAGGTG	ATCCAACCAC	CCTGGCCTCC	CAAAGTGCTG	GGATTATAGG	4860
CGTGAGCCAC	AGCGCCTGGC	CTGAAGCAGC	CACTCACTTT	TACAGACCCT	AAGACAATGA	4920
TTGCAAGCTG	GTAGGATTGC	TGTTTGCCCC	ACCCAGCTGC	GGTGTGAGT	TTGGGTGCGG	4980
TCTCCTGTGC	TTTGCACCTG	GCCCGCTTAA	GGCATTTGTT	ACCCGTAATG	CTCCTGTAAG	5040
GCATCTGCGT	TTGTGACATC	GTTTTGGTCG	CCAGGAAGGG	ATTGGGGCTC	TAAGCTTGAG	5100
CGGTTCATCC	TTTTCATTTA	TACAGGGGAT	GACCAGAGTC	ATTGGCGCTA	TGGAGGTGAG	5160
ACACCCACCC	GCTGCACAGA	CCCAATCTGG	GAACCCAGCT	CTGTGGATCT	CCCCTACAGC	5220
CGTCCCTGAA	CACTGGTCCC	GGGCGTCCCA	CCCGCCGCCC	ACCGTCCCAC	CCCCTCACCT	5280
TTTCTACCCG	GGTTCCTTAA	GTTCTTGACC	TAGGCGTCAG	ACTTCCTCAC	TATACTCTCC	5340
CACCCAGGC	GACCCGCCCT	GGCCCCGGGT	GTCCCCAGCC	TGCGCGGGCC	GCTTCCAGTC	5400

CCCGGTGGAT	ATCCGCCCCC	AGCTCGCCGC	CTTCTGCCCC	GCCCTGCGCC	CCCTGGAACT	5460
CCTGGGCTTC	CAGCTCCCGC	CGCTCCCAGA	ACTGCGCCTG	CGCAACAATG	GCCACAGTGG	5520
TGAGGGGGTC	TCCCCGCCGA	GACTTGGGGA	TGGGGCGGGG	CGCAGGGAAG	GGAACCGTCG	5580
CGCAGTGCCT	GCCCCGGGGT	TGGGCTGGCC	CTACCGGGCG	GGGCCGGCTC	ACTTGCCTCT	5640
CCCTACGCAG	TGCAACTGAC	CCTGCCTCCT	GGGCTAGAGA	TGGCTCTGGG	TCCCCGGGCGG	5700
GAGTACCGGG	CTCTGCAGCT	GCATCTGCAC	TGGGGGGCTG	CAGGTCGTCC	GGGCTCGGAG	5760
CACACTGTGG	AAGGCCACCG	TTTCCCTGCC	GAGGTGAGCG	CGGACTGGCC	GAGAAGGGGC	5820
AAAGGAGCGG	GGCGGACGGG	GGCCAGAGAC	GTGGCCCTCT	CCTACCCTCG	TGTCCTTTTC	5880
AGATCCACGT	GGTTCACCTC	AGCACCGCCT	TTGCCAGAGT	TGACGAGGCC	TTGGGGCGCC	5940
CGGGAGGCCT	GGCCGTGTTG	GCCGCCTTTC	TGGAGGTACC	AGATCCTGGA	CACCCCCTAC	6000
TCCCCGCTTT	CCCATCCCAT	GCTCCTCCCG	GACTCTATCG	TGGAGCCAGA	GACCCCATCC	6060
CAGCAAGCTC	ACTCAGGCCC	CTGGCTGACA	AACTCATTCA	CGCACTGTTT	GTTCATTTAA	6120
CACCCACTGT	GAACCAGGCA	CCAGCCCCCA	ACAAGGATTC	TGAAGCTGTA	GGTCCTTGCC	6180
TCTAAGGAGC	CCACAGCCAG	TGGGGGAGGC	TGACATGACA	GACACATAGG	AAGGACATAG	6240
TAAAGATGGT	GGTCACAGAG	GAGGTGACAC	TTAAAGCCTT	CACTGGTAGA	AAAGAAAAGG	6300
AGGTGTTTCAT	TGCAGAGGAA	ACAGAATGTG	CAAAGACTCA	GAATATGGCC	TATTTAGGGA	6360
ATGGCTACAT	ACACCATGAT	TAGAGGAGGC	CCAGTAAAGG	GAAGGGATGG	TGAGATGCCT	6420
GCTAGGTTCA	CTCACTCACT	TTTATTTATT	TATTTATTTT	TTTGACAGTC	TCTCTGTCGC	6480
CCAGGCTGGA	GTGCAGTGGT	GTGATCTTGG	GTCACTGCAA	CTTCCGCCTC	CCGGGTTCAA	6540
GGGATTCTCC	TGCCTCAGCT	TCCTGAGTAG	CTGGGGTTAC	AGGTGTGTGC	CACCATGCCC	6600
AGCTAATTTT	TTTTTGTATT	TTTAGTAGAC	AGGGTTTCAC	CATGTTGGTC	AGGCTGGTCT	6660
CAAACCTCTG	GCCTCAAGTG	ATCCGCCTGA	CTCAGCCTAC	CAAAGTGCTG	ATTACAAGTG	6720
TGAGCCACCG	TGCCCAGCCA	CACTCACTGA	TTCTTTAATG	CCAGCCACAC	AGCACAAAGT	6780
TCAGAGAAAT	GCCTCCATCA	TAGCATGTCA	ATATGTTTCAT	ACTCTTAGGT	TCATGATGTT	6840
CTTAACATTA	GGTTCATAAG	CAAAATAAGA	AAAAAGAATA	ATAAATAAAA	GAAGTGGCAT	6900
GTCAGGACCT	CACCTGAAAA	GCCAAACACA	GAATCATGAA	GGTGAATGCA	GAGGTGACAC	6960
CAACACAAAG	GTGTATATAT	GGTTTCCTGT	GGGGAGTATG	TACGGAGGCA	GCAGTGAGTG	7020
AGACTGCAAA	CGTCAGAAGG	GCACGGGTCA	CTGAGAGCCT	AGTATCCTAG	TAAAGTGGGC	7080

TCTCTCCCTC	TCTCTCCAGC	TTGTCATTGA	AAACCAGTCC	ACCAAGCTTG	TTGGTTCGCA	7140
CAGCAAGAGT	ACATAGAGTT	TGAAATAATA	CATAGGATTT	TAAGAGGGAG	ACACTGTCTC	7200
TAAAAAAAAA	AACAACAGCA	ACAACAAAAA	GCAACAACCA	TTACAATTTT	ATGTTCCCTC	7260
AGCATTCTCA	GAGCTGAGGA	ATGGGAGAGG	ACTATGGGAA	CCCCCTTCAT	GTTCCGGCCT	7320
TCAGCCATGG	CCCTGGATAC	ATGCACTCAT	CTGTCTTACA	ATGTCATTCC	CCCAGGAGGG	7380
CCCGGAAGAA	AACAGTGCCT	ATGAGCAGTT	GCTGTCTCGC	TTGGAAGAAA	TCGCTGAGGA	7440
AGGTCAGTTT	GTTGGTCTGG	CCACTAATCT	CTGTGGCCTA	G TTCATAAAG	AATCACCTT	7500
TGGAGCTTCA	GGTCTGAGGC	TGGAGATGGG	CTCCCTCCAG	TGCAGGAGGG	ATTGAAGCAT	7560
GAGCCAGCGC	TCATCTTGAT	AATAACCATG	AAGCTGACAG	ACACAGTTAC	CCGCAAACGG	7620
CTGCCTACAG	ATTGAAAACC	AAGCAAAAAC	CGCCGGGCAC	GGTGGCTCAC	GCCTGTAATC	7680
CCAGCACTTT	GGGAGGCCAA	GGCAGGTGGA	TCACGAGGTC	AAGAGATCAA	GACCATCCTG	7740
GCCAACATGG	TGAAACCCCA	TCTCTACTAA	AAATACGAAA	AAATAGCCAG	GCGTGGTGGC	7800
GGGTGCCTGT	AATCCCAGCT	ACTCGGGAGG	CTGAGGCAGG	AGAATGGCAT	GAACCCGGGA	7860
GGCAGAAGTT	GCAGTGAGCC	GAGATCGTGC	CACTGCACTC	CAGCCTGGGC	AACAGAGCGA	7920
GACTCTTGTC	TCAAAAAAAAA	AAAAAAAAAA	GAAAACCAAG	CAAAAACCAA	AATGAGACAA	7980
AAAAACAAG	ACCAAAAAAT	GGTGTTTGGA	AATTGTCAAG	GTCAAGTCTG	GAGAGCTAAA	8040
CTTTTTCTGA	GAAGTGTTTA	TCTTTAATAA	GCATCAAATA	TTTTAACTTT	GTAAATACTT	8100
TTGTTGGAAA	TCGTTCTCTT	CTTAGTCACT	CTTGGGTCAT	TTTAAATCTC	ACTTACTCTA	8160
CTAGACCTTT	TAGGTTTCTG	CTAGACTAGG	TAGAACTCTG	CCTTTGCATT	TCTTGTGTCT	8220
GTTTTGTATA	GTTATCAATA	TTCATATTTA	TTTACAAGTT	ATTCAGATCA	TTTTTTCTTT	8280
TCTTTTTTTT	TTTTTTTTTT	TTTTTTACAT	CTTTAGTAGA	GACAGGGTTT	CACCATATTG	8340
GCCAGGCTGC	TCTCAAACCTC	CTGACCTTGT	GATCCACCAG	CCTCGGCCTC	CCAAAGTGCT	8400
GGGATTCATT	TTTTCTTTTT	AATTGCTCT	GGGCTTAAAC	TTGTGGCCCA	GCACTTTATG	8460
ATGGTACACA	GAGTTAAGAG	TGTAGACTCA	GACGGTCTTT	CTTCTTTCCT	TCTCTTCCTT	8520
CCTCCCTTCC	CTCCACCTT	CCCTTCTCTC	CTTCCTTTCT	TTCTTCCTCT	CTTGCTTCCT	8580
CAGGCCTCTT	CCAGTTGCTC	CAAAGCCCTG	TACTTTTTTT	TGAGTTAACG	TCTTATGGGA	8640
AGGGCCTGCA	CTTAGTGAAG	AAGTGGTCTC	AGAGTTGAGT	TACCTTGGCT	TCTGGGAGGT	8700
GAAACTGTAT	CCCTATACCC	TGAAGCTTTA	AGGGGGTGCA	ATGTAGATGA	GACCCCAACA	8760

TAGATCCTCT	TCACAGGCTC	AGAGACTCAG	GTCCCAGGAC	TGGACATATC	TGCACTCCTG	8820
CCCTCTGACT	TCAGCCGCTA	CTTCCAATAT	GAGGGGTCTC	TGACTACACC	GCCCTGTGCC	8880
CAGGGTGTCA	TCTGGACTGT	GTTTAACCAG	ACAGTGATGC	TGAGTGCTAA	GCAGGTGGGC	8940
CTGGGGTGTG	TGTGGACACA	GTGGGTGCGG	GGGAAAGAGG	ATGTAAGATG	AGATGAGAAA	9000
CAGGAGAAGA	AAGAAATCAA	GGCTGGGCTC	TGTGGCTTAC	GCCTATAATC	CCACCACGTT	9060
GGGAGGCTGA	GGTGGGAGAA	TGGTTTGAGC	CCAGGAGTTC	AAGACAAGGC	GGGGCAACAT	9120
AGTGTGACCC	CATCTCTACC	AAAAAAACCC	CAACAAAACC	AAAAATAGCC	GGGCATGGTG	9180
GTATGCGGCC	TAGTCCCAGC	TACTCAAGGA	GGCTGAGGTG	GGAAGATCGC	TTGATTCCAG	9240
GAGTTTGAGA	CTGCAGTGAG	CTATGATCCC	ACCACTGCCT	ACCATCTTTA	GGATACATTT	9300
ATTTATTTAT	AAAAGAAATC	AAGAGGCTGG	ATGGGGAATA	CAGGAGCTGG	AGGGTGGAGC	9360
CCTGAGGTGC	TGGTTGTGAG	CTGGCCTGGG	ACCCTTGTTT	CCTGTCATGC	CATGAACCCA	9420
CCCACACTGT	CCACTGACCT	CCCTAGCTCC	ACACCCTCTC	TGACACCCTG	TGGGGACCTG	9480
GTGACTCTCG	GCTACAGCTG	AACTTCCGAG	CGACGCAGCC	TTTGAATGGG	CGAGTGATTG	9540
AGGCCTCCTT	CCCTGCTGGA	GTGGACAGCA	GTCCTCGGGC	TGCTGAGCCA	GGTACAGCTT	9600
TGTCTGGTTT	CCCCCAGCC	AGTAGTCCCT	TATCCTCCCA	TGTGTGTGCC	AGTGTCTGTC	9660
ATTGGTGGTC	ACAGCCCGCC	TCTCACATCT	CCTTTTTCTC	TCCAGTCCAG	CTGAATTCCT	9720
GCCTGGCTGC	TGGTGAGTCT	GCCCCTCCTC	TTGGTCCTGA	TGCCAGGAGA	CTCCTCAGCA	9780
CCATTGAGCC	CCAGGGCTGC	TCAGGACCGC	CTCTGCTCCC	TCTCCTTTTC	TGCAGAACAG	9840
ACCCCAACCC	CAATATTAGA	GAGGCAGATC	ATGGTGGGGA	TTCCCCCATT	GTCCCCAGAG	9900
GCTAATTGAT	TAGAATGAAG	CTTGAGAAAT	CTCCCAGCAT	CCCTCTCGCA	AAAGAATCCC	9960
CCCCCCTTTT	TTTAAAGATA	GGGTCTCACT	CTGTTTGCCC	CAGGCTGGGG	TGTTGTGGCA	10020
CGATCATAGC	TCACTGCAGC	CTCGAACTCC	TAGGCTCAGG	CAATCCTTTC	ACCTTAGCTT	10080
CTCAAAGCAC	TGGGACTGTA	GGCATGAGCC	ACTGTGCCTG	GCCCCAAACG	GCCCTTTTAC	10140
TTGGCTTTTA	GGAAGCAAAA	ACGGTGCTTA	TCTTACCCCT	TCTCGTGTAT	CCACCCTCAT	10200
CCCTTGCTG	GCCTCTTCTG	GAGACTGAGG	CACTATGGGG	CTGCCTGAGA	ACTCGGGGCA	10260
GGGGTGGTGG	AGTGCACTGA	GGCAGGTGTT	GAGGAACTCT	GCAGACCCCT	CTTCCTTCCC	10320
AAAGCAGCCC	TCTCTGCTCT	CCATCGCAGG	TGACATCCTA	GCCCTGGTTT	TTGGCCTCCT	10380
TTTTGCTGTC	ACCAGCGTCG	CGTTCCTTGT	GCAGATGAGA	AGGCAGCACA	GGTATTACAC	10440

TGACCCTTTC TTCAGGCACA AGCTTCCCCC ACCCTTGTGG AGTCACTTCA TGCAAAGCGC 10500
 ATGCAAATGA GCTGCTCCTG GGCCAGTTTT CTGATTAGCC TTTCCTGTTG TGTACACACA 10560
 GAAGGGGAAC CAAAGGGGGT GTGAGCTACC GCCCAGCAGA GGTAGCCGAG ACTGGAGCCT 10620
 AGAGGCTGGA TCTTGGAGAA TGTGAGAAGC CAGCCAGAGG CATCTGAGGG GGAGCCGTA 10680
 ACTGTCCTGT CCTGCTCATT ATGCCACTTC CTTTAACTG CCAAGAAATT TTTTAAAATA 10740
 AATATTTATA ATAAAATATG TGTTAGTCAC CTTTGTTCCC CAAATCAGAA GGAGGTATTT 10800
 GAATTTCTTA TTAGTGTTAT TAGCACCAAT TTAGTGGTAA TGCATTTATT CTATTACAGT 10860
 TCGGCCTCCT TCCACACATC ACTCCAATGT GTTGCTCC 10898

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (A) DESCRIPTION: Signal peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met	Ala	Pro	Leu	Cys	Pro	Ser	Pro	Trp	Leu	Pro	Leu	Leu	Ile	Pro	Ala
1				5					10					15	
Pro	Ala	Pro	Gly	Leu	Thr	Val	Gln	Leu	Leu	Leu	Ser	Leu	Leu	Leu	Leu
			20					25					30		
Met	Pro	Val	His	Pro											
			35												

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer"

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

TGGGGTTCTT GAGGATCTCC AGGAG

25

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer"

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

CTCTAACTTC AGGGAGCCCT CTTCTT

26

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer"

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

(D) OTHER INFORMATION: N stands for inosine

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

CUACUACUAC UAGGCCACGC GTCGACTAGT ACGGGNNGGG NNGGGNNG

48

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Glu Glu Asp Leu Pro Ser
1 5

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION:55..60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Gly Glu Asp Asp Pro Leu
1 5

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Asn Asn Ala His Arg Asp Lys Glu Gly Asp Asp Gln Ser His Trp Arg
1 5 10 15
Tyr Gly Gly Asp Pro
20

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION:36..51

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

His	Pro	Gln	Arg	Leu	Pro	Arg	Met	Gln	Glu	Asp	Ser	Pro	Leu	Gly	Gly
1				5					10					15	

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Glu	Glu	Asp	Ser	Pro	Arg	Glu	Glu	Asp	Pro	Pro	Gly	Glu	Glu	Asp	Leu
1				5					10					15	

Pro	Gly	Glu	Glu	Asp	Leu	Pro	Gly
							20

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION:279..291

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

Leu	Glu	Glu	Gly	Pro	Glu	Glu	Asn	Ser	Ala	Tyr	Glu	Gln
1				5					10			

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Met	Arg	Arg	Gln	His	Arg	Arg	Gly	Thr	Lys	Gly	Gly	Val	Ser	Tyr	Arg
1				5					10					15	

(2) INFORMATION FOR SEQ ID NO: 17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

GTCGCTAGCT CCATGGGTCA TATGCAGAGG TTGCCCCGGA TGCAG

45

(2) INFORMATION FOR SEQ ID NO: 18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

GAAGATCTCT TACTCGAGCA TTCTCCAAGA TCCAGCCTCT AGG

43

(2) INFORMATION FOR SEQ ID NO: 19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULAR TYPE: DNA (genomic)

- (A) DESCRIPTION: AP-2 transcription factor

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TCCCCCACCC

10

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULAR TYPE: DNA (genomic)

(A) DESCRIPTION: initiator (Inr) element

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CCACCCCCAT

10

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULAR TYPE: DNA (genomic)

(A) DESCRIPTION: p53 binding site

(x) PUBLICATION INFORMATION:

- (A) AUTHORS: El Deiry et al.
- (B) TITLE: "Human genomic DNA sequences define a consensus binding site for p53"
- (C) JOURNAL: Nature Genetics
- (D) VOLUME: 1
- (F) PAGES: 44-49
- (G) DATE: 1992

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

AAGCTAGTCC

10

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Leu Glu His His His His His His
1 5

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) DESCRIPTION: Initiator consensus sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

YYYCAYYYYY

10

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) DESCRIPTION: p53 binding site

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(x) PUBLICATION INFORMATION:

- (A) AUTHORS: El Deiry et al.
- (B) TITLE: "Human genomic DNA sequences define a
consensus binding site for p53"
- (C) JOURNAL: Nature Genetics
- (D) VOLUME: 1
- (F) PAGES: 44-49
- (G) DATE: 1992

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

AGGCTTGCTC

10

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

Ser Pro Xaa Xaa

1

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Thr Pro Xaa Xaa

1

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) DESCRIPTION: Proposed MN promoter

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

CTTGCTTTTC ATTCAAGCTC AAGTTTGTCT CCCACATACC CATTACTTAA CTCACCCTCG	60
GGCTCCCCTA GCAGCCTGCC CTACCTCTTT ACCTGCTTCC TGGTGGAGTC AGGGATGTAT	120
ACATGAGCTG CTTTCCCTCT CAGCCAGAGG ACATGGGGGG CCCCAGCTCC CCTGCCTTTC	180
CCCTTCTGTG CCTGGAGCTG GGAAGCAGGC CAGGGTTAGC TGAGGCTGGC TGGCAAGCAG	240
CTGGGTGGTG CCAGGGAGAG CCTGCATAGT GCCAGGTGGT GCCTTGGGTT CCAAGCTAGT	300
CCATGGCCCC GATAACCTTC TGCCTGTGCA CACACCTGCC CCTCACTCCA CCCCATCCT	360

AGCTTTGGTA TGGGGGAGAG GGCACAGGGC CAGACAAACC TGTGAGACTT TGGCTCCATC 420
TCTGCAAAAG GGCGCTCTGT GAGTCAGCCT GCTCCCCTCC AGGCTTGCTC CTCCCCCACC 480
CAGCTCTCGT TTCCAATGCA CGTACAGCCC GTACACACCG TGTGCTGGGA CACCCCACAG 540

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 445 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (A) DESCRIPTION: 1st MN exon

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

GCCCGTACAC ACCGTGTGCT GGGACACCCC ACAGTCAGCC GCATGGCTCC CCTGTGCCCC 60
AGCCCCTGGC TCCCTCTGTT GATCCCGGCC CCTGCTCCAG GCCTCACTGT GCAACTGCTG 120
CTGTCACTGC TGCTTCTGGT GCCTGTCCAT CCCCAGAGGT TGCCCCGGAT GCAGGAGGAT 180
TCCCCCTTGG GAGGAGGCTC TTCTGGGGAA GATGACCCAC TGGGCGAGGA GGATCTGCCC 240
AGTGAAGAGG ATTCACCCAG AGAGGAGGAT CCACCCGGAG AGGAGGATCT ACCTGGAGAG 300
GAGGATCTAC CTGGAGAGGA GGATCTACCT GAAGTTAAGC CTAAATCAGA AGAAGAGGGC 360
TCCCTGAAGT TAGAGGATCT ACCTACTGTT GAGGCTCCTG GAGATCCTCA AGAACCCAG 420
AATAATGCCC ACAGGGACAA AGAAG 445

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (A) DESCRIPTION: 2nd MN exon

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

GGGATGACCA GAGTCATTGG CGCTATGGAG

30

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) DESCRIPTION: 3rd MN exon

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

GCGACCCGCC CTGGCCCCGG GTGTCCCCAG CCTGCGCGGG CCGCTTCCAG TCCCCGGTGG 60

ATATCCGCCC CCAGCTCGCC GCCTTCTGCC CGGCCCTGCG CCCCTGGAA CTCCTGGGCT 120

TCCAGCTCCC GCCGCTCCCA GAACTGCGCC TGC GCAACAA TGGCCACAGT G 171

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) DESCRIPTION: 4th MN exon

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

TGCAACTGAC CCTGCCTCCT GGGCTAGAGA TGGCTCTGGG TCCCGGGCGG GAGTACCGGG 60

CTCTGCAGCT GCATCTGCAC TGGGGGGCTG CAGGTCGTCC GGGCTCGGAG CACACTGTGG 120

AAGGCCACCG TTTCCCTGCC GAG 143

(2) INFORMATION FOR SEQ ID NO: 32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 93 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) DESCRIPTION: 5th MN exon

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

ATCCACGTGG TTCACCTCAG CACCGCCTTT GCCAGAGTTG ACGAGGCCTT GGGGCGCCCG 60

GGAGGCCTGG CCGTGTTGGC CGCCTTTCTG GAG 93

(2) INFORMATION FOR SEQ ID NO: 33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 67 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) DESCRIPTION: 6th MN exon

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

GAGGGCCCGG AAGAAAACAG TGCCTATGAG CAGTTGCTGT CTCGCTTGA AGAAATCGCT 60

GAGGAAG 67

(2) INFORMATION FOR SEQ ID NO: 34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 158 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) DESCRIPTION: 7th MN exon

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

GCTCAGAGAC TCAGGTCCCA GGACTGGACA TATCTGCACT CCTGCCCTCT GACTTCAGCC	60
GCTACTTCCA ATATGAGGGG TCTCTGACTA CACCGCCCTG TGCCCAGGGT GTCATCTGGA	120
CTGTGTTTAA CCAGACAGTG ATGCTGAGTG CTAAGCAG	158

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (A) DESCRIPTION: 8th MN exon

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

CTCCACACCC TCTCTGACAC CCTGTGGGGA CCTGGTGACT CTCGGCTACA GCTGAACTTC	60
CGAGCGACGC AGCCTTTGAA TGGGCGAGTG ATTGAGGCCT CCTTCCCTGC TGGAGTGGAC	120
AGCAGTCCTC GGGCTGCTGA GCCAG	145

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (A) DESCRIPTION: 9th MN exon

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

TCCAGCTGAA TTCCTGCCTG GCTGCTG	27
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(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) DESCRIPTION: 10th MN exon

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

GTGACATCCT AGCCCTGGTT TTTGGCCTCC TTTTGTCTGT CACCAGCGTC GCGTTCCTTG 60

TGCAGATGAG AAGGCAGCAC AG 82

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) DESCRIPTION: 11th MN exon

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

AAGGGGAACC AAAGGGGGTG TGAGCTACCG CCCAGCAGAG GTAGCCGAGA CTGGAGCCTA 60

GAGGCTGGAT CTTGGAGAAT GTGAGAAGCC AGCCAGAGGC ATCTGAGGGG GAGCCGGTAA 120

CTGTCCTGTC CTGCTCATTA TGCCACTTCC TTTTAACTGC CAAGAAATTT TTTAAAATAA 180

ATATTTATAA T 191

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1174 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) DESCRIPTION: 1st MN intron

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

GTAAGTGGTC ATCAATCTCC AAATCCAGGT TCCAGGAGGT TCATGACTCC CCTCCCATAC	60
CCCAGCCTAG GCTCTGTTCA CTCAGGGAAG GAGGGGAGAC TGTACTCCCC ACAGAAGCCC	120
TTCCAGAGGT CCCATACCAA TATCCCCATC CCCACTCTCG GAGGTAGAAA GGGACAGATG	180
TGGAGAGAAA ATAAAAAGGG TGCAAAAGGA GAGAGGTGAG CTGGATGAGA TGGGAGAGAA	240
GGGGGAGGCT GGAGAAGAGA AAGGGATGAG AACTGCAGAT GAGAGAAAAA ATGTGCAGAC	300
AGAGGAAAAA AATAGGTGGA GAAGGAGAGT CAGAGAGTTT GAGGGGAAGA GAAAAGGAAA	360
GCTTGGGAGG TGAAGTGGGT ACCAGAGACA AGCAAGAAGA GCTGGTAGAA GTCATCTCAT	420
CTTAGGCTAC AATGAGGAAT TGAGACCTAG GAAGAAGGGA CACAGCAGGT AGAGAAACGT	480
GGCTTCTTGA CTCCAAGCC AGGAATTTGG GGAAAGGGGT TGGAGACCAT ACAAGGCAGA	540
GGGATGAGTG GGGAGAAGAA AGAAGGGAGA AAGGAAAGAT GGTGTACTCA CTCATTTGGG	600
ACTCAGGACT GAAGTGCCCA CTCACTTTTT TTTTTTTTTT TTTTGAGACA AACTTTCACT	660
TTTGTGCCCC AGGCTGGAGT GCAATGGCGC GATCTCGGCT CACTGCAACC TCCACCTCCC	720
GGGTTCAAGT GATTCTCCTG CCTCAGCCTC TAGCCAAGTA GCTGCGATTA CAGGCATGCG	780
CCACCACGCC CGGCTAATTT TTGTATTTTT AGTAGAGACG GGGTTTCGCC ATGTTGGTCA	840
GGCTGGTCTC GAACTCCTGA TCTCAGGTGA TCCAACCACC CTGGCCTCCC AAAGTGCTGG	900
GATTATAGGC GTGAGCCACA GCGCCTGGCC TGAAGCAGCC ACTCACTTTT ACAGACCCTA	960
AGACAATGAT TGCAAGCTGG TAGGATTGCT GTTTGGCCCA CCCAGCTGCG GTGTTGAGTT	1020
TGGGTGCGGT CTCCTGTGCT TTGCACCTGG CCCGCTTAAG GCATTTGTTA CCCGTAATGC	1080
TCCTGTAAGG CATCTGCGTT TGTGACATCG TTTTGGTCGC CAGGAAGGGA TTGGGGCTCT	1140
AAGCTTGAGC GGTTCATCCT TTTCATTTAT ACAG	1174

(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) DESCRIPTION: 2nd MN intron

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

GTGAGACACC CACCCGCTGC ACAGACCCAA TCTGGGAACC CAGCTCTGTG GATCTCCCCT	60
ACAGCCGTCC CTGAACACTG GTCCCGGGCG TCCCACCCGC CGCCACCGT CCCACCCCCT	120
CACCTTTTCT ACCCGGGTTC CCTAAGTTCC TGACCTAGGC GTCAGACTTC CTCACTATAC	180
TCTCCCACCC CAG	193

(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) DESCRIPTION: 3rd MN intron

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

GTGAGGGGGT CTCCCCGCCG AGACTTGGGG ATGGGGCGGG GCGCAGGGAA GGGAACCGTC	60
GCGCAGTGCC TGCCCGGGGG TTGGGCTGGC CCTACCGGGC GGGGCCGGCT CACTTGCCTC	120
TCCCTACGCA G	131

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) DESCRIPTION: 4th MN intron

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

GTGAGCGCGG ACTGGCCGAG AAGGGGCAAA GGAGCGGGGC GGACGGGGGC CAGAGACGTG	60
GCCCTCTCCT ACCCTCGTGT CCTTTTCAG	89

(2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) DESCRIPTION: 5th MN intron

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

GTACCAGATC CTGGACACCC CCTACTCCCC GCTTTCCCAT CCCATGCTCC TCCCGGACTC	60
TATCGTGGAG CCAGAGACCC CATCCCAGCA AGCTCACTCA GGCCCTGGC TGACAAACTC	120
ATTCACGCAC TGTTTGTTCA TTTAACACCC ACTGTGAACC AGGCACCAGC CCCCACAAG	180
GATTCTGAAG CTGTAGGTCC TTGCCTCTAA GGAGCCCACA GCCAGTGGGG GAGGCTGACA	240
TGACAGACAC ATAGGAAGGA CATAGTAAAG ATGGTGGTCA CAGAGGAGGT GACACTTAAA	300
GCCTTCACTG GTAGAAAAGA AAAGGAGGTG TTCATTGCAG AGGAAACAGA ATGTGCAAAG	360
ACTCAGAATA TGGCCTATTT AGGGAATGGC TACATACACC ATGATTAGAG GAGGCCAGT	420
AAAGGGAAGG GATGGTGAGA TGCCTGCTAG GTTCACTCAC TCACTTTTAT TTATTTATTT	480
ATTTTTTTTGA CAGTCTCTCT GTCGCCCAGG CTGGAGTGCA GTGGTGTGAT CTTGGGTCAC	540
TGCAACTTCC GCCTCCCGGG TTCAAGGGAT TCTCCTGCCT CAGCTTCCTG AGTAGCTGGG	600
GTTACAGGTG TGTGCCACCA TGCCCAGCTA ATTTTTTTTT GTATTTTATG TAGACAGGGT	660
TTCACCATGT TGGTCAGGCT GGTCTCAAAC TCCTGGCCTC AAGTGATCCG CCTGACTCAG	720
CCTACCAAAG TGCTGATTAC AAGTGTGAGC CACCGTGCCC AGCCACACTC ACTGATTCTT	780
TAATGCCAGC CACACAGCAC AAAGTTCAGA GAAATGCCTC CATCATAGCA TGTCAATATG	840
TTCATACTCT TAGGTTTCATG ATGTTCTTAA CATTAGGTTC ATAAGCAAAA TAAGAAAAAA	900

.GAATAATAAA TAAAAGAAGT GGCATGTCAG GACCTCACCT GAAAAGCCAA ACACAGAATC	960
ATGAAGGTGA ATGCAGAGGT GACACCAACA CAAAGGTGTA TATATGGTTT CCTGTGGGGA	1020
GTATGTACGG AGGCAGCAGT GAGTGAGACT GCAAACGTCA GAAGGGCACG GGTCACTGAG	1080
AGCCTAGTAT CCTAGTAAAG TGGGCTCTCT CCCTCTCTCT CCAGCTTGTC ATTGAAAACC	1140
AGTCCACCAA GCTTGTGTTGGT TCGCACAGCA AGAGTACATA GAGTTTGAAA TAATACATAG	1200
GATTTTAAGA GGGAGACACT GTCTCTAAAA AAAAAACAA CAGCAACAAC AAAAAGCAAC	1260
AACCATTACA ATTTTATGTT CCCTCAGCAT TCTCAGAGCT GAGGAATGGG AGAGGACTAT	1320
GGGAACCCCC TTCATGTTCC GGCCTTCAGC CATGGCCCTG GATACATGCA CTCATCTGTC	1380
TTACAATGTC ATTCCCCCAG	1400

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1334 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (A) DESCRIPTION: 6th MN intron

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

GTCAGTTTGT TGGTCTGGCC ACTAATCTCT GTGGCCTAGT TCATAAAGAA TCACCCTTTG	60
GAGCTTCAGG TCTGAGGCTG GAGATGGGCT CCCTCCAGTG CAGGAGGGAT TGAAGCATGA	120
GCCAGCGCTC ATCTTGATAA TAACCATGAA GCTGACAGAC ACAGTTACCC GCAAACGGCT	180
GCCTACAGAT TGAAAACCAA GCAAAAACCG CCGGGCACGG TGGCTCACGC CTGTAATCCC	240
AGCACTTTGG GAGGCCAAGG CAGGTGGATC ACGAGGTCAA GAGATCAAGA CCATCCTGGC	300
CAACATGGTG AAACCCCATC TCTACTAAAA ATACGAAAAA ATAGCCAGGC GTGGTGGCGG	360
GTGCCTGTAA TCCCAGCTAC TCGGGAGGCT GAGGCAGGAG AATGGCATGA ACCCGGGAGG	420
CAGAAGTTGC AGTGAGCCGA GATCGTGCCA CTGCACTCCA GCCTGGGCAA CAGAGCGAGA	480
CTCTTGTCTC AAAAAAAAAA AAAAAAAGA AAACCAAGCA AAAACCAAAA TGAGACAAAA	540
AAAACAAGAC CAAAAAATGG TGTTTGGAAA TTGTCAAGGT CAAGTCTGGA GAGCTAAACT	600

TTTCTGAGA ACTGTTTATC TTTAATAAGC ATCAAATATT TTAAC TTTGT AAATACTTTT	660
GTTGGAAATC GTTCTCTTCT TAGTCACTCT TGGGTCATTT TAAATCTCAC TTACTCTACT	720
AGACCTTTTA GGT TTTCTGCT AGACTAGGTA GAACTCTGCC TTTGCATTTT TTGTGTCTGT	780
TTTGTATAGT TATCAATATT CATATTTATT TACAAGTTAT TCAGATCATT TTTTCTTTTC	840
TTTTTTTTTT TTTTTTTTTT TTTTACATCT TTAGTAGAGA CAGGGTTTCA CCATATTGGC	900
CAGGCTGCTC TCAAACCTCT GACCTTGTGA TCCACCAGCC TCGGCCTCCC AAAGTGCTGG	960
GATTCATTTT TTCTTTTAA TTTGCTCTGG GCTTAAACTT GTGGCCCAGC ACTTTATGAT	1020
GGTACACAGA GTTAAGAGTG TAGACTCAGA CGGTCTTTCT TCTTTCCTTC TCTTCCTTCC	1080
TCCCTTCCCT CCCACCTTCC CTTCTCTCCT TCCTTTCTTT CTCCTCTCT TGCTTCCTCA	1140
GGCCTCTTCC AGTTGCTCCA AAGCCCTGTA CTTTTTTTTT AGTTAACGTC TTATGGGAAG	1200
GGCCTGCACT TAGTGAAGAA GTGGTCTCAG AGTTGAGTTA CCTTGGCTTC TGGGAGGTGA	1260
AACTGTATCC CTATACCCTG AAGCTTTAAG GGGGTGCAAT GTAGATGAGA CCCCAACATA	1320
GATCCTCTTC ACAG	1334

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (A) DESCRIPTION: 7th MN intron

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

GTGGGCCTGG GGTGTGTGTG GACACAGTGG GTGCGGGGGA AAGAGGATGT AAGATGAGAT	60
GAGAAACAGG AGAAGAAAGA AATCAAGGCT GGGCTCTGTG GCTTACGCCT ATAATCCCAC	120
CACGTTGGGA GGCTGAGGTG GGAGAATGGT TTGAGCCCAG GAGTTCAAGA CAAGGCGGGG	180
CAACATAGTG TGACCCCATC TCTACCAAAA AAACCCCAAC AAAACCAAAA ATAGCCGGGC	240
ATGGTGGTAT GCGGCCTAGT CCCAGCTACT CAAGGAGGCT GAGGTGGGAA GATCGCTTGA	300
TTCCAGGAGT TTGAGACTGC AGTGAGCTAT GATCCCACCA CTGCCTACCA TCTTTAGGAT	360

ACATTTATTT ATTTATAAAA GAAATCAAGA GGCTGGATGG GGAATACAGG AGCTGGAGGG	420
TGGAGCCCTG AGGTGCTGGT TGTGAGCTGG CCTGGGACCC TTGTTTCCTG TCATGCCATG	480
AACCCACCCA CACTGTCCAC TGACCTCCCT AG	512

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (A) DESCRIPTION: 8th MN intron

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

GTACAGCTTT GTCTGGTTTC CCCCAGCCA GTAGTCCCTT ATCCTCCCAT GTGTGTGCCA	60
GTGTCTGTCA TTGGTGGTCA CAGCCCGCCT CTCACATCTC CTTTTTCTCT CCAG	114

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 617 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (A) DESCRIPTION: 9th MN intron

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

GTGAGTCTGC CCCTCCTCTT GGTCTGATG CCAGGAGACT CCTCAGCACC ATTCAGCCCC	60
AGGGCTGCTC AGGACCGCCT CTGCTCCCTC TCCTTTTCTG CAGAACAGAC CCCAACCCCA	120
ATATTAGAGA GGCAGATCAT GGTGGGGATT CCCCATTGT CCCCAGAGGC TAATTGATTA	180
GAATGAAGCT TGAGAAATCT CCCAGCATCC CTCTCGCAAA AGAATCCCCC CCCCTTTTTT	240
TAAAGATAGG GTCTCACTCT GTTTGCCCA GGCTGGGGTG TTGTGGCAGC ATCATAGCTC	300

.ACTGCAGCCT CGAACTCCTA GGCTCAGGCA ATCCTTTCAC CTTAGCTTCT CAAAGCACTG	360
GGACTGTAGG CATGAGCCAC TGTGCCTGGC CCCAAACGGC CCTTTTACTT GGCTTTTAGG	420
AAGCAAAAAC GGTGCTTATC TTACCCCTTC TCGTGTATCC ACCCTCATCC CTTGGCTGGC	480
CTCTTCTGGA GACTGAGGCA CTATGGGGCT GCCTGAGAAC TCGGGGCAGG GGTGGTGGAG	540
TGCACTGAGG CAGGTGTTGA GGA ACTCTGC AGACCCCTCT TCCTTCCCAA AGCAGCCCTC	600
TCTGCTCTCC ATCGCAG	617

(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (A) DESCRIPTION: 10th MN intron

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

GTATTACACT GACCCTTTCT TCAGGCACAA GCTTCCCCCA CCCTTGTGGA GTCACTTCAT	60
GCAAAGCGCA TGCAAATGAG CTGCTCCTGG GCCAGTTTTC TGATTAGCCT TTCCTGTTGT	120
GTACACACAG	130

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1401 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (A) DESCRIPTION: Spans 3' part of 1st intron to beyond
end of 5th exon

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

CAAAC TTTCA CTTTT GTTGC CCAGG CTGGA GTGCA ATGGC GCGAT CTCGG CTCAC TGCAA	60
CCTCC ACCTC CCGGG TTCAA GTGAT TCTCC TGCCT CAGCC TCTAG CCAAG TAGCT GCGAT	120
TACAG GCATG CGCCAC CACG CCCGG CTAAT TTTTG TATTT TTAGT AGAGA CGGGG TTTTCG	180
CCATG TTGGT CAGGCT GGTG TCGAA CTCCT GATCT CAGGT GATCC AACCA CCCTG GCCTC	240
CCAAAG TGCT GGGAT TATAG GCGTG AGCCA CAGCG CCTGG CCTGA AGCAG CCACT CACTT	300
TTACAG ACCC TAAGAC AATG ATTGC AAGCT GGTAG GATTG CTGTT TTGGC CACCC AGCTG	360
CGGTG TTGAG TTTGG GTGCG GTCTC CTGTG CTTTG CACCT GGCCC GCTTA AGGCAT TTTGT	420
TACCCG TAAT GCTCCT GTAA GGCAT CTGCG TTTGT GACAT CGTTTT TGGTC GCCAG GAAGG	480
GATTG GGGCT CTAAG CTTGA GCGGT TCATC CTTTT CATTT ATACAG GGGG TGACC AGAGT	540
CATTG GCGCT ATGGAG GTGA GACACC CACC CGCTG CACAG ACCCA ATCTG GGAACC CAGC	600
TCTGT GGATC TCCCCT ACAG CCGTC CCTGA AACTG GTTCC CGGGC GTCCC ACCCG CCCGCC	660
CACCG TCCA CCCCCT CACC TTTTCT ACCC GGGTT CCCTA AGTTC CTGAC CTAGG CGTCA	720
GACTT CCTCA CTATA CTCT CCACCC CAGG CGACCC GCCC TGGCCCC GGG TGTCCCC CAGC	780
CTGCG CGGGC CGCTT CCAGT CCCC GGTTGA TATCC GCCCC CAGCT CGCCG CCTTCT GCCC	840
GGCCCT GCGC CCCCT GGAAC TCCTG GGCTT CCAGCT CCCG CCGCT CCCAG AACTG CGCCT	900
GCGCA ACAAT GGCCAC AGTG GTGAG GGGGT CTCCCC GCCG AGACT TGGGG ATGGGG CGGG	960
GCGCAG GGAA GGAAC CGTC GCGCA GTGCC TGCCC GGGGG TTGGG CTGGC CCTACC GGGC	1020
GGGGC CGGCT CACTT GCCTC TCCCT ACGCA GTGCA ACTGA CCCTG CCTCC TGGGCT AGAG	1080
ATGGCT CTGG GTCCC GGGCG GGAGT ACCGG GCTCT GCAGC TGCAT CTGCA CTGGGG GGGCT	1140
GCAGGT CGTC CGGGCT CGGA GCACACT GTG GAAGGCC ACC GTTTC CCTGC CGAGGT GAGC	1200
GCGGACT GGC CGAGA AGGGG CAAAG GAGCG GGGCG GACGG GGGCC AGAGA CGTGG CCCCTC	1260
TCCTACC CTC GTGTC CTTTT CAGAT CCACG TGGTT CACCT CAGCA CCGCC TTTGCC AGAG	1320
TTGAC GAGGC CTTGG GGGCG CCGGG AGGCC TGGCC GTGTT GGCCG CCCTT CTGGAG GTAC	1380
CAGATC CTGG ACACCCC CTA C	1401

(2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(A) DESCRIPTION: Region of homology to collagen alpha
1 chain

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

Gln	Arg	Leu	Pro	Arg	Met	Gln	Glu	Asp	Ser	Pro	Leu	Gly	Gly	Gly	Ser	
1				5					10					15		
Ser	Gly	Glu	Asp	Asp	Pro	Leu	Gly	Glu	Glu	Asp	Leu	Pro	Ser	Glu	Glu	
			20					25					30			
Asp	Ser	Pro	Arg	Glu	Glu	Asp	Pro	Pro	Gly	Glu	Glu	Asp	Leu	Pro	Gly	
		35					40					45				
Glu	Glu	Asp	Leu	Pro	Gly	Glu	Glu	Asp	Leu	Pro	Glu	Val	Lys	Pro	Lys	
	50					55					60					
Ser	Glu	Glu	Glu	Gly	Ser	Leu	Lys	Leu	Glu	Asp	Leu	Pro	Thr	Val	Glu	
65					70					75					80	
Ala	Pro	Gly	Asp	Pro	Gln	Glu	Pro	Gln	Asn	Asn	Ala	His	Arg	Asp	Lys	
				85					90					95		
Glu	Gly															

(2) INFORMATION FOR SEQ ID NO: 51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(A) DESCRIPTION: carbonic anhydrase domain

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

Asp	Asp	Gln	Ser	His	Trp	Arg	Tyr	Gly	Gly	Asp	Pro	Pro	Trp	Pro	Arg	
1				5					10					15		
Val	Ser	Pro	Ala	Cys	Ala	Gly	Arg	Phe	Gln	Ser	Pro	Val	Asp	Ile	Arg	
			20					25					30			
Pro	Gln	Leu	Ala	Ala	Phe	Cys	Pro	Ala	Leu	Arg	Pro	Leu	Glu	Leu	Leu	
		35					40					45				
Gly	Phe	Gln	Leu	Pro	Pro	Leu	Pro	Glu	Leu	Arg	Leu	Arg	Asn	Asn	Gly	
	50					55				60						
His	Ser	Val	Gln	Leu	Thr	Leu	Pro	Pro	Gly	Leu	Glu	Met	Ala	Leu	Gly	
65					70					75					80	

Pro	Gly	Arg	Glu	Tyr	Arg	Ala	Leu	Gln	Leu	His	Leu	His	Trp	Gly	Ala	85	90	95	
Ala	Gly	Arg	Pro	Gly	Ser	Glu	His	Thr	Val	Glu	Gly	His	Arg	Phe	Pro	100	105	110	
Ala	Glu	Ile	His	Val	Val	His	Leu	Ser	Thr	Ala	Phe	Ala	Arg	Val	Asp	115	120	125	
Glu	Ala	Leu	Gly	Arg	Pro	Gly	Gly	Leu	Ala	Val	Leu	Ala	Ala	Phe	Leu	130	135	140	
Glu	Glu	Gly	Pro	Glu	Glu	Asn	Ser	Ala	Tyr	Glu	Gln	Leu	Leu	Ser	Arg	145	150	155	160
Leu	Glu	Glu	Ile	Ala	Glu	Glu	Gly	Ser	Glu	Thr	Gln	Val	Pro	Gly	Leu	165	170	175	
Asp	Ile	Ser	Ala	Leu	Leu	Pro	Ser	Asp	Phe	Ser	Arg	Tyr	Phe	Gln	Tyr	180	185	190	
Glu	Gly	Ser	Leu	Thr	Thr	Pro	Pro	Cys	Ala	Gln	Gly	Val	Ile	Trp	Thr	195	200	205	
Val	Phe	Asn	Gln	Thr	Val	Met	Leu	Ser	Ala	Lys	Gln	Leu	His	Thr	Leu	210	215	220	
Ser	Asp	Thr	Leu	Trp	Gly	Pro	Gly	Asp	Ser	Arg	Leu	Gln	Leu	Asn	Phe	225	230	235	240
Arg	Ala	Thr	Gln	Pro	Leu	Asn	Gly	Arg	Val	Ile	Glu	Ala	Ser	Phe	Pro	245	250	255	

(2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

- (A) DESCRIPTION: transmembrane region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

Ile	Leu	Ala	Leu	Val	Phe	Gly	Leu	Leu	Phe	Ala	Val	Thr	Ser	Val	Ala	1	5	10	15
Phe	Leu	Val	Gln													20			

(2) INFORMATION FOR SEQ ID NO: 53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) DESCRIPTION: intracellular C-terminus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

Met	Arg	Arg	Gln	His	Arg	Arg	Gly	Thr	Lys	Gly	Gly	Val	Ser	Tyr	Arg
1				5					10					15	
Pro	Ala	Glu	Val	Ala	Glu	Thr	Gly	Ala							
			20					25							

(2) INFORMATION FOR SEQ ID NO: 54:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 170 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

Arg	Ala	Leu	Gln	Leu	His	Leu	His	Trp	Gly	Ala	Ala	Gly	Arg	Pro	Gly
1				5					10					15	
Ser	Glu	His	Thr	Val	Glu	Gly	His	Arg	Phe	Pro	Ala	Glu	Ile	His	Val
			20					25					30		
Val	His	Leu	Ser	Thr	Ala	Phe	Ala	Arg	Val	Asp	Glu	Ala	Leu	Gly	Arg
		35					40					45			
Pro	Gly	Gly	Leu	Ala	Val	Leu	Ala	Ala	Phe	Leu	Glu	Glu	Gly	Pro	Glu
	50					55					60				
Glu	Asn	Ser	Ala	Tyr	Glu	Gln	Leu	Leu	Ser	Arg	Leu	Glu	Glu	Ile	Ala
65					70					75				80	
Glu	Glu	Gly	Ser	Glu	Thr	Gln	Val	Pro	Gly	Leu	Asp	Ile	Ser	Ala	Leu
			85						90					95	
Leu	Pro	Ser	Asp	Phe	Ser	Arg	Tyr	Phe	Gln	Tyr	Glu	Gly	Ser	Leu	Thr
			100					105					110		
Thr	Pro	Pro	Cys	Ala	Gln	Gly	Val	Ile	Trp	Thr	Val	Phe	Asn	Gln	Thr
		115					120					125			
Val	Met	Leu	Ser	Ala	Lys	Gln	Leu	His	Thr	Leu	Ser	Asp	Thr	Leu	Trp
	130					135						140			

Gly	Pro	Gly	Asp	Ser	Arg	Leu	Gln	Leu	Asn	Phe	Arg	Ala	Thr	Gln	Pro
145					150					155					160
Leu	Asn	Gly	Arg	Val	Ile	Glu	Ala	Ser	Phe						
				165					170						

(2) INFORMATION FOR SEQ ID NO: 55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

CAUGGCCCCG AUAACCUUCU GCCUGUGCAC ACACCUGCCC CUCACUCCAC CCCCAUCCUA	60
GCUUUGGUAU GGGGGAGAGG GCACAGGGCC AGACAAACCU GUGAGACUUU GGCUCCAUCU	120
CUGCAAAAGG GCGCUCUGUG AGUCAGCCUG CUCCCCUCCA GGCUUGCUCU UCCCCACCC	180
AGCUCUCGUU UCCAAUGCAC GUACAGCCCG UACACACCGU GUGCUGGGAC ACCCCACAGU	240
CAGCCGCAUG GCUCCCCUGU GCCCCAGCCC CUGGCUCCCU CUGUUGAUCC CGGCCCCUGC	300
UCCAGGCCUC ACUGUGCAAC UGCUGCUGUC ACUGCUGCUU CUGGUGCCUG UCCAUCCCCA	360
GAGGUUGCCC CGGAUGCAGG AGGAUUCCCC CUUGGGAGGA GGCUCUUCUG GGGAAGAUGA	420
CCCACUGGGC GAGGAGGAUC UGCCAGUGA AGAGGAUUA CCCAGAGAGG	470

(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

This sequence is intentionally skipped.

(2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

This sequence is intentionally skipped.

(2) INFORMATION FOR SEQ ID NO: 58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 904 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

GCTGGTCTCG AACTCCTGGA CTCAAGCAAT CCACCCACCT CAGCCTCCCA AAATGAGGGA	60
CCGTGTCTTA TTCATTCCA TGTCCCTAGT CCATAGCCCA GTGCTGGACC TATGGTAGTA	120
CTAAATAAAT ATTTGTTGAA TGCAATAGTA AATAGCATTT CAGGGAGCAA GAACTAGATT	180
AACAAAGGTG GTAAAAGGTT TGGAGAAAAA AATAATAGTT TAATTTGGCT AGAGTATGAG	240
GGAGAGTAGT AGGAGACAAG ATGGAAAGGT CTCTTGGGCA AGGTTTTGAA GGAAGTTGGA	300
AGTCAGAAGT ACACAATGTG CATATCGTGG CAGGCAGTGG GGAGCCAATG AAGGCTTTTG	360
AGCAGGAGAG TAATGTGTTG AAAAATAAAT ATAGGTTAAA CCTATCAGAG CCCCTCTGAC	420
ACATACACTT GCTTTTCATT CAAGCTCAAG TTTGTCTCCC ACATACCCAT TACTTAACTC	480
ACCCTCGGGC TCCCCTAGCA GCCTGCCCTA CCTCTTTACC TGCTTCCTGG TGGAGTCAGG	540
GATGTATACA TGAGCTGCTT TCCCTCTCAG CCAGAGGACA TGGGGGGCCC CAGCTCCCCT	600
GCCTTTCCCC TTCTGTGCCT GGAGCTGGGA AGCAGGCCAG GGTTAGCTGA GGCTGGCTGG	660
CAAGCAGCTG GGTGGTGCCA GGGAGAGCCT GCATAGTGCC AGGTGGTGCC TTGGGTTCCA	720
AGCTAGTCCA TGGCCCCGAT AACCTTCTGC CTGTGCACAC ACCTGCCCCT CACTCCACCC	780
CCATCCTAGC TTTGGTATGG GGGAGAGGGC ACAGGGCCAG ACAAACCTGT GAGACTTTGG	840
CTCCATCTCT GCAAAAGGGC GCTCTGTGAG TCAGCCTGCT CCCCTCCAGG CTTGCTCCTC	900
CCCC	904

(2) INFORMATION FOR SEQ ID NO: 59:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 292 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

TTTTTTTGAG ACGGAGTCTT GCATCTGTCA TGCCCAGGCT GGAGTAGCAG TGGTGCCATC	60
TCGGCTCACT GCAAGCTCCA CCTCCCGAGT TCACGCCATT TTCCTGCCTC AGCCTCCCGA	120
GTAGCTGGGA CTACAGGCGC CCGCCACCAT GCCCGGCTAA TTTTTGTAT TTTTGGTAGA	180
GACGGGGTTT CACCGTGTTA GCCAGAATGG TCTCGATCTC CTGACTTCGT GATCCACCCG	240
CCTCGGCCTC CCAAAGTTCT GGGATTACAG GTGTGAGCCA CCGCACCTGG CC	292

(2) INFORMATION FOR SEQ ID NO: 60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

TTCTTTTTTG AGACAGGGTC TTGCTCTGTC ACCCAGGCCA GAGTGCAATG GTACAGTCTC	60
AGCTCACTGC AGCCTCAACC GCCTCGGCTC AAACCATCAT CCCATTTTCAG CCTCCTGAGT	120
AGCTGGGACT ACAGGCACAT GCCATTACAC CTGGCTAATT TTTTTGTATT TCTAGTAGAG	180
ACAGGGTTTG GCCATGTTGC CCGGGCTGGT CTCGAACTCC TGGACTCAAG CAATCCACCC	240
ACCTCAGCCT CCCAAAATGA GG	262

(2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

TTTTTTTTTTG AGACAAACTT TCACTTTTGT TGCCCAGGCT GGAGTGCAAT GGCGCGATCT	60
CGGCTCACTG CAACCTCCAC CTCCCGGGTT CAAGTGATTC TCCTGCCTCA GCCTCTAGCC	120
AAGTAGCTGC GATTACAGGC ATGCGCCACC ACGCCCGGCT AATTTTTGTA TTTTGTAGTAG	180
AGACGGGGTT TCGCCATGTT GGTCAGGCTG GTCTCGAACT CCTGATCTCA GGTGATCCAA	240
CCACCCTGGC CTCCCAAAGT GCTGGGATTA TAGGCGTGAG CCACAGCGCC TGGC	294

(2) INFORMATION FOR SEQ ID NO: 62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

TGACAGTCTC TCTGTCGCCC AGGCTGGAGT GCAGTGGTGT GATCTTGGGT CACTGCAACT	60
TCCGCCTCCC GGGTTCAAGG GATTCTCCTG CCTCAGCTTC CTGAGTAGCT GGGGTTACAG	120
GTGTGTGCCA CCATGCCCAG CTAATTTTTT TTTGTATTTT TAGTAGACAG GGTTTCACCA	180
TGTTGGTCAG GCTGGTCTCA AACTCCTGGC CTCAAGTGAT CCGCCTGACT CAGCCTACCA	240
AAGTGCTGAT TACAAGTGTG AGCCACCGTG CCCAGC	276

(2) INFORMATION FOR SEQ ID NO: 63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

CGCCGGGCAC GGTGGCTCAC GCCTGTAATC CCAGCACTTT GGGAGGCCAA GGCAGGTGGA	60
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TCACGAGGTC AAGAGATCAA GACCATCCTG GCCAACATGG TGAAACCCCA TCTCTACTAA	120
AAATACGAAA AAATAGCCAG GCGTGGTGGC GGGTGCCTGT AATCCCAGCT ACTCGGGAGG	180
CTGAGGCAGG AGAATGGCAT GAACCCGGA GGCAGAAGTT GCAGTGAGCC GAGATCGTGC	240
CACTGCACTC CAGCCTGGGC AACAGAGCGA GACTCTTGTC TCAAAAAAA	289

(2) INFORMATION FOR SEQ ID NO: 64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

AGGCTGGGCT CTGTGGCTTA CGCCTATAAT CCCACCACGT TGGGAGGCTG AGGTGGGAGA	60
ATGGTTTGAG CCCAGGAGTT CAAGACAAGG CGGGGCAACA TAGTGTGACC CCATCTCTAC	120
CAAAAAAACC CCAACAAAAC CAAAAATAGC CGGGCATGGT GGTATGCGGC CTAGTCCCAG	180
CTACTCAAGG AGGCTGAGGT GGGAAGATCG CTTGATTCCA GGAGTTTGAG ACTGCAGTGA	240
GCTATGATCC CACCACTGCC TACCATCTTT AGGATACATT TATTTATTTA TAAAAGAA	298

(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

TTTTTTACAT CTTTAGTAGA GACAGGGTTT CACCATATTG GCCAGGCTGC TCTCAAACCTC	60
CTGACCTTGT GATCCACCAG CCTCGGCCTC CCAAAGTGCT GGGAT	105

(2) INFORMATION FOR SEQ ID NO: 66:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 83 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

CCTCGAACTC CTAGGCTCAG GCAATCCTTT CACCTTAGCT TCTCAAAGCA CTGGGACTGT 60

AGGCATGAGC CACTGTGCCT GGC 83

(2) INFORMATION FOR SEQ ID NO: 67:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) DESCRIPTION: 5' donor consensus splice sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

AGAAGGTAAG T 11

(2) INFORMATION FOR SEQ ID NO: 68:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) DESCRIPTION: 5' donor consensus splice sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

TGGAGGTGAG A 11

(2) INFORMATION FOR SEQ ID NO: 69:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 base pairs
 - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) DESCRIPTION: 5' donor consensus splice sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

CAGTCGTGAG G

11

(2) INFORMATION FOR SEQ ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) DESCRIPTION: 5' donor consensus splice sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

CCGAGGTGAG C

11

(2) INFORMATION FOR SEQ ID NO: 71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) DESCRIPTION: 5' donor consensus splice sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

TGGAGGTACC A

11

(2) INFORMATION FOR SEQ ID NO: 72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) DESCRIPTION: 5' donor consensus splice sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

GGAAGGTCAG T

11

(2) INFORMATION FOR SEQ ID NO: 73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) DESCRIPTION: 5' donor consensus splice sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

AGCAGGTGGG C

11

(2) INFORMATION FOR SEQ ID NO: 74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) DESCRIPTION: 5' donor consensus splice sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

GCCAGGTACA G

11

(2) INFORMATION FOR SEQ ID NO: 75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) DESCRIPTION: 5' donor consensus splice sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

TGCTGGTGAG T

11

(2) INFORMATION FOR SEQ ID NO: 76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) DESCRIPTION: 5' donor consensus splice sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

CACACGGTATT A

11

(2) INFORMATION FOR SEQ ID NO: 77:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) DESCRIPTION: 3' acceptor consensus splice sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

ATACAGGGGA T

11

(2) INFORMATION FOR SEQ ID NO: 78:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) DESCRIPTION: 3' acceptor consensus splice sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

CCCCAGGCGA C

11

(2) INFORMATION FOR SEQ ID NO: 79:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) DESCRIPTION: 3' acceptor consensus splice sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

ACGCAGTGCA A

11

(2) INFORMATION FOR SEQ ID NO: 80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) DESCRIPTION: 3' acceptor consensus splice sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

TTTCAGATCC A

11

(2) INFORMATION FOR SEQ ID NO: 81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) DESCRIPTION: 3' acceptor consensus splice sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

CCCCAGGAGG G

11

(2) INFORMATION FOR SEQ ID NO: 82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) DESCRIPTION: 3' acceptor consensus splice sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

TCACAGGCTC A

11

(2) INFORMATION FOR SEQ ID NO: 83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) DESCRIPTION: 3' acceptor consensus splice sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

CCCTAGCTCC A

11

(2) INFORMATION FOR SEQ ID NO: 84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) DESCRIPTION: 3' acceptor consensus splice sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

CTCCAGTCCA G

11

(2) INFORMATION FOR SEQ ID NO: 85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) DESCRIPTION: 3' acceptor consensus splice sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

TCGCAGGTGA CA

12

(2) INFORMATION FOR SEQ ID NO: 86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) DESCRIPTION: 3' acceptor consensus splice sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

ACACAGAAGG G